

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: COHEN, Maurice  
FRIEDMAN, Paula N.  
GORDON, Julian  
HODGES, Steven C.  
KLASS, Michael R.  
KRATOCHVIL, Jon D.  
ROBERTS-RAPP, Lisa  
RUSSELL, John C.  
STROUPE, Steven D.
- (ii) TITLE OF THE INVENTION: REAGENTS AND METHODS USEFUL  
FOR DETECTING DISEASES OF THE PROSTATE
- (iii) NUMBER OF SEQUENCES: 35
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Abbott Laboratories  
(B) STREET: 100 Abbott Park Road  
(C) CITY: Abbott Park  
(D) STATE: IL  
(E) COUNTRY: USA  
(F) ZIP: 60064-3500
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Becker, Cheryl L.  
(B) REGISTRATION NUMBER: 35,441  
(C) REFERENCE/DOCKET NUMBER: 5697.US.P1
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 847/935-1729  
(B) TELEFAX: 847/938-2623  
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 367 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGCGCNGGAG	CCTGAGCGGA	GGGTGTGCGC	AGCCTCGCCA	GCGGGGGGCC	CGGGCTGNGC	60
CATTGCCTCA	CTGAGCCAGC	GCCTGCCTNC	TACCTCGCCG	ACAGCTGGAA	CCAGTGCGAC	120
CTAGTGGCTC	TCACCTGCTT	CCTCCTGGGC	GTGGGCTGCC	GGCTGACCCC	GGGTTTGTAC	180
CACCTGGGCC	GCACTGTCCT	CTGCATCGAC	TTCATGGTTT	TCACGGTGCG	GCTGCTTCAC	240
ATCTTCACGG	TCAACAAACA	GCTGGGGCCC	AAGATCGTCA	TCGTGAGCAA	GATGATGAAG	300
GACGTGTTCT	TCTTCCTCTT	CTTCCTCGGC	GTGTGGCTGG	TAGCTATGGG	TTGGGCCACG	360
GAGGGGT						367

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CAAACAGCTG	GGGCCCAAGA	TCGTATCGT	GAGCAAGATG	ATGAAGGACG	TGTTCTTCTT	60
CCTCTTCTTC	CTCGGCGTGT	GGCTGGTAGC	CTATGGCGTG	GCCACGGAGG	GGCTCCTGAG	120
GCCACGGGAC	AGTGACTTCC	CAAGTATCCT	GCGCCGCGTC	TTCTACCGTC	CCTACCTGCA	180
GATCTTCGGG	CAGATTCCCC	AGGAGGACAT	GGAC			214

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGTGTGGCTG	GTAGCCTATG	GCGTGGCCAC	GGAGGGGCTC	CTGAGGCCAC	GGGACAGTGA	60
CTTCCCAAGT	ATCCTGCGCC	GCGTCTTCTA	CCGTCCCTAC	CTGCAGATCT	TCGGGCAGAT	120
TCCCCAGGAG	GACATGGACG	TGGCCCTCAT	GGAGCACAGC	AACTGCTCGT	CGGAGCCCGG	180
CTTCTGGGCA	CACCCTCCTG	GGGCC				205

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGGCAGATT	CCCCAGGAGG	ACATGGACGT	GGCCCTCATG	GAGCACAGCA	ACTGCTCGTC	60
GGAGCCCGGC	TTCTGGGCAC	ACCCTCCTGG	GGCCCAGGCG	GGCACCTGCG	TCTCCAGTA	120
TGCCAACTGG	CTGGTGGTGC	TGCTCCTCGT	CATCTTCCTG	CTCGTGGCCA	ACATCCTGCT	180
GGTCAACTTG	CTCATTGCCA	TGTTCACTTA	CACATTCGGC	AAAGTACAGG	GCAACAGCGA	240
TCTCTACTGG	AAGGCG					256

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCGATCTCTA	CTGGAAGGCG	CAGGTTACCG	CCTCATCCGG	GAATTCCACT	CTCGGCCCCG	60
GCTGGCCCCG	CCCTTTATCG	TCATCTCCCA	CTTGCGCCTC	CTGCTCAGGC	AATTGTGCAG	120
GCGACCCCGG	AGCCCCCAGC	CGTCTCCCC	GGCCCTCGAG	CATTTCCGGG	TTTACCTTTC	180
TAAGGAAGCC	GAGCGGAAGC	TGCTAACGTG	GGAATCGGTG	CATAAGGAGA	ACTTTCTGCT	240
GGCAGC						246

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTGCATAAGG	AGAACTTTCT	GCTGGCACGC	GCTAGGGACA	AGCGGGAGAG	CGACTCCGAG	60
CGTCTGAAGC	GCACGTCCCA	GAAGGTGGAC	TTGGCACTGA	AACAGCTGGG	ACACATCCGC	120
GAGTACGAAC	AGCGCCTGAA	AGTGCTGGAG	CGGGAGGTCC	AGCAGTGTAG	CCGCGTCCTG	180
GGGTGGGTGG	CCGAGGCCCT	GAGCCGCTCT	GCCTTGCTGC	CCCCAGGTGG	GCCGCCACCC	240
CCTGACCTGC	CTGGGTCCAA	AGACTGAGCC	CTGCTGG			277

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGGTCCAAAG	ACTGANCCCT	GCTGGCGGAC	TTCAAGGAGA	AGCCCCCACA	GGGGATTTTG	60
CTCCTAGAGT	AAGGCTCATC	TGGGCCTCGG	CCCCCGCACC	TGGTGGCCTT	GTCCTTGAGG	120
TGAGCCCCAT	GTCCATCTGG	GCCACTGTCA	GGACCACCTT	TGGGAGTGTC	ATCCTTACAA	180
ACCACAGCAT	GCCCCGGCTC	TCCCAGAACC	AGTCCCAGCC	TGGGAGGATC	AAGGCCTGGA	240
TCCCCGGGCC	T					251

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGCTCATCTG	GGCCTCGGCC	CCCGCACCTG	GTGGCCTTGT	CCTTGAGGTG	AGCCCCATGT	60
CCATCTGGGC	CACTGTCAGG	ACCACCTTTG	GGAGTGTGTC	CCTTACAAAC	CACAGCATGC	120
CCGGCTCCTC	CCAGAACCAG	TCCCAGCCTG	GGAGGATCAA	GGCCTGGATC	CCGGGCCGTT	180
ATCCATCTGG	AGGCTGCAGG	GTCCTTGGGG	TAACAGGGAC	CAC		223

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAGGCCACCT	CGCCGCTCTC	CTGGATGCTG	GCCTCGGCAG	GCCCCCTGAA	CCTGCTTCTT	60
TGGGCACTGT	TGCTGAAACA	GGCACAGATG	GCCATGTACT	TCTGGGAGAT	GGGTTCCAAT	120
GCAGTTTCTT	CAGCTCTTGG	GGCCTGTTTG	CTGCTCCGGG	TGATGGCACG	CCTGGAGCCT	180
GACGCTGAGG	AGGCAGCACG	GAGGAAAGAC	CTGGCGTTCA	AGTTTGAGGG	GATGGGCGTT	240
GACCTCTTTG	GCGAGTGCTA	TCGCAGCAGT	GAGGTGAGGG	CTGCCCCCCT	CCTCCTCCGT	300
CGYTGCCCGC	TCTGGGGGGA	TGCCACTTTG	CCTTCCAGGT	GGCCATGCAA	AGCTGACGSC	360
CSTGMCTTCT	TTGCCMAGGA	TGGGGTACAG	TCTCTGCTGA	CACAGAAAGT	GTGGGGAGAT	420
ATGGCCAGCA	CTACACCCAT	CTGGGCCCTG	GTTATCGCGT	TCTTTTGCCC	TCCACTCATC	480
TACACCCGCC	TCATCACCTT	CAGGAAATCA	GAAGAGGAGC	CCACACGGGA	GGAGCTAGAG	540
TTTGACATGG	ATAGTGTGAT	TAATGGGGAA	GGGCCTGTG	GGACGGCGGA	CCCAGCCGAG	600
AAGACGCCGC	TGGGGGTCCC	GCGCCAGTCG	GGCCGTCCGG	GTTGCTGCGG	GGGCCGCTGC	660
GGGGGGCGCC	GGTGCCACG	CCGCTGGTTC	CACCTCTGGG	GCGCGCCGGT	GACCATCTTC	720
ATGGGCAACG	TGGTCAGCTA	CCTGCTGTTT	CTGCTGCTTT	TCTCGCGGGT	GCTGCTCGTG	780
GATTTCCAGC	CGGCGCCGCC	CGGCTCCCTG	GAGCTGCTGC	TCTATTTCTG	GGCTTTACAG	840
CTGCTGTGCG	AGGAATGCGC	CAGGGCCTGA	GCGGAGGCGG	GGGCAGCCTC	GCCAGCGGGG	900
GCCCCGGGCC	TGGCCATGCC	TCACTGAGCC	AGCGCCTGCG	CCTCTACCTC	GCCGACAGCT	960
GGAAACCATG	CGACCTAGTG	GCTCTCACCT	GCTTCTCCTT	GGGCGTGGG	TGCCGGCTGA	1020
CCCCGGGTTT	GTACCACCTG	GGCCGCACTG	TCCTCTGCAT	CGACTTCATG	GTTTTACCGG	1080
TGCGGCTGCT	TCACATCTTC	ACGGTCAACA	AACAGCTGGG	GCCCAAGATC	GTCATCGTGA	1140
GCAAGATGAT	GAAGGACGTG	TTCTTCTTCC	TCTTCTTCTT	CGGCGTGTGG	CTGGTAGCCT	1200
ATGGCGTGCG	CACGGAGGGG	CTCCTGAGGC	CACGGGACAG	TGACTTCCCA	AGTATCCTGC	1260
GCCGCGTCTT	TACCCGTCCC	TACCTGCAGA	TCTTCGGGCA	GATTCCCCAG	GAGGACATGG	1320
ACGTGGCCCT	CATGGAGCAC	AGCAACTGCT	CGTCGGAGCC	CGGCTTCTGG	GCACACCCTC	1380
CTGGGGCCCA	GGCGGGCACC	TGCGTCTCCC	AGTATGCCAA	CTGGCTGGTG	GTGCTGCTCC	1440
TCGTATCTTT	CCTGCTCGTG	GCCAACATCC	TGCTGGTCAA	CTTGCTCATT	GCCATGTTCA	1500
GTTACACATT	CGGCAAAGTA	CAGGGCAACA	GCGATCTCTA	CTGGAAGGCG	CAGGTTACCG	1560
CCTCATCCGG	GAATTCCACT	CTCGGCCCGC	GCTGGCCCCG	CCCTTTATCG	TCATCTCCCA	1620
CTTGCGCCTC	CTGCTCAGGC	AATTGTGCAG	GCGACCCCGG	AGCCCCCAGC	CGTCTCTCCC	1680
GGCCCTCGAG	CATTTCCGGG	TTTACCTTTC	TAAGGAAGCC	GAGCGGAAGC	TGCTAACGTG	1740
GGAATCGGTG	CATAAGGAGA	ACTTTCTGCT	GGCACGCGCT	AGGGACAAGC	GGGAGAGCGA	1800
CTCCGAGCGT	CTGAAGCGCA	CGTCCCGAGA	GGTGGACTTG	GCATGAAAC	AGCTGGGACA	1860
CATCCGCGAG	TACGAACAGC	GCCTGAAAGT	GCTGGAGCGG	GAGGTCCAGC	AGGTAGCCG	1920
CGTCTTGGGG	TGGGTGGCCG	AGGCCCTGAG	CCGCTCTGCC	TTGCTGCCCC	CAGGTGGGCC	1980
GCCACCCCTT	GACCTGCCTG	GGTCCAAAGA	CTGAGCCCTG	CTGGCGGACT	TCAAGGAGAA	2040
GCCCCACAG	GGGATTTTGC	TCCTAGAGTA	AGGCTCATCT	GGGCCTCGGG	CCCCGCACCT	2100
GGTGGCCCTT	TCCTTGAGGT	GAGCCCCATG	TCCATCTGGG	CCACTGTCAG	GACCACTTTT	2160
GGGAGTGTCA	TCCTTACAAA	CCACAGCATG	CCCGGCTCCT	CCCAGAACCA	GTCCCAGCCT	2220
GGGAGGATCA	AGGCCTGGAT	CCCGGGCCGT	TATCCATCTG	GAGGCTGCAG	GGTCTTTGGG	2280
GTAACAGGGA	CCACAGACCC	CTCACCCTC	ACAGATTCCT	CACACTGGGG	AAATAAAGCC	2340
ATTTTCAGAG	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	GGGCGGCCGC	GGT	2393

(2). INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAATTCGGCT	CGAGCAAACA	GCTGGGGCCC	AAGATCGTCA	TCGTGAGCAA	GATGATGAAG	60
GACGTGTTCT	TCTTCTCTTT	CTTCTCTCGG	GTGTGGCTGG	TAGCCTATGG	CGTGGCCACG	120
GAGGCGCTCC	TGAGGCCACG	GGACAGTGAC	TTCCCAAGTA	TCCTGCGCCG	CGTCTTCTAC	180
CGTCCCTACC	TGCAGATCTT	CGGGCAGATT	CCCCAGGAGG	ACATGGACGT	GGCCCTCATG	240
GAGCACAGCA	ACTGCTCGTC	GGAGCCCCGG	TTCTGGGCAC	ACCCTCCTGG	GGCCCAGGCG	300
GGCACCTGCG	TCTCCAGTA	TGCCAACTGG	CTGGTGGTGC	TGCTCCTCGT	CATCTTCTCT	360
CTCGTGGCCA	ACATCTGCT	GGTCAACTTG	CTCATTTGCA	TGTTTCACTA	CACATTCCGC	420
AAAGTACAGG	GCAACAGCGA	TCTCTACTGG	AAGGCGCAGC	GTTACCCGCT	CATCCGGGAA	480
TTCCACTCTC	GGCCCCGCGT	GGCCCCGCCC	TTTATCGTCA	TCTCCCACTT	GCGCCTCCTG	540
CTCAGGCAAT	TGTGCAGGCG	ACCCCGGAGC	CCCCAGCCGT	CCTCCCCGGC	CCTCGAGCAT	600

TTCCGGGTTT	ACCTTTCTAA	GGAAGCCGAG	CGGAAGCTGC	TAACGTGGGA	ATCGGTGCAT	660
AAGGAGAACT	TTCTGCTGGC	ACGCGCTAGG	GACAAGCGGG	AGAGCGACTC	CGAGCGTCTG	720
AAGCGCACGT	CCCAGAAGGT	GGACTTGGA	CTGAAACAGC	TGGGACACAT	CCGCGAGTAC	780
GAACAGCGCC	TGAAAGTGCT	GGAGCGGGAG	GTCCAGCAGT	GTAGCCGCGT	CCTGGGGTGG	840
GTGGCCGAGG	CCCTGAGCCG	CTCTGCCTTG	CTGCCCCCAG	GTGGGCCCGCC	ACCCCCCTGAC	900
CTGCCTGGGT	CCAAAGACTG	AGCCCTGCTG	GCGGACTTCA	AGGAGAAGCC	CCCACAGGGG	960
ATTTTGCTCC	TAGAGTAAGG	CTCATCTGGG	CCTCGGCCCC	CGCACCTGGT	GGCCTTGTC	1020
TTGAGGTGAG	CCCCATGTCC	ATCTGGGCCA	CTGTCAGGAC	CACCTTTGGG	AGTGTCATCC	1080
TTACAAACCA	CAGCATGCCC	GGCTCCTCCC	AGAACCAGTC	CCAGCCTGGG	AGGATCAAGG	1140
CCTGGATCCC	GGGCCGTTAT	CCATCTGGAG	GCTGCAGGGT	CCTTGGGGTA	ACAGGGACCA	1200
CAGACCCCTC	ACCACTCACA	GATTCCTCAC	ACTGGGGAAA	TAAAGCCATT	TCAGAGGAAA	1260
AAAAAAAAAA	AAAAAAAAAA	AAAAAAGGG	CGGCCGC			1297

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGCTCGGAAT	TCCGAGCTTG	GATCCTCTAG	AGCGGCCGCC	GACTAGTGAG	CTCGTCGACC	60
CGGGAATT						68

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AATTAATTCC	CGGGTCGACG	AGCTCACTAG	TCGGCGGCCG	CTCTAGAGGA	TCCAAGCTCG	60
GAATTCCG						68

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGCGGATAAC	AATTCACAC	AGGA	24
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(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGTAACACGA	CGGCCAGT	18
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(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ACTGGCTGGT GGTGCTGC

18

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TCCCAGAAGG TGGACTTGGC

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCTTGAGGTG AGCCCCAT

18

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TGCTGTGGTT TGTAAGGAT

19

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TTCCGCTCGG CTTCTTAGA

20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCAGCACCAC CAGCCAGTTG

20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TCTTCTTCCT CTTCTTCCTC

20

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTGTTGCCCT GTACTTTG

18

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCCGCCATGA AACAGCTGGG GCCCAAGAT

29

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCGGCCGCCG TCTTTGGACC CAGGC

25

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Lys	Ala	Thr	Ser	Pro	Leu	Ser	Trp	Met	Leu	Ala	Ser	Ala	Gly	Pro	Leu
1				5					10					15	
Asn	Leu	Leu	Leu	Trp	Ala	Leu	Leu	Leu	Lys	Gln	Ala	Gln	Met	Ala	Met
			20					25					30		
Tyr	Phe	Trp	Glu	Met	Gly	Ser	Asn	Ala	Val	Ser	Ser	Ala	Leu	Gly	Ala
		35					40					45			
Cys	Leu	Leu	Leu	Arg	Val	Met	Ala	Arg	Leu	Glu	Pro	Asp	Ala	Glu	Glu
	50					55					60				
Ala	Ala	Arg	Arg	Lys	Asp	Leu	Ala	Phe	Lys	Phe	Glu	Gly	Met	Gly	Val
65					70					75					80
Asp	Leu	Phe	Gly	Glu	Cys	Tyr	Arg	Ser	Ser	Glu	Val	Arg	Ala	Ala	Arg
			85						90					95	
Leu	Leu	Leu	Arg	Arg	Cys	Pro	Leu	Trp	Gly	Asp	Ala	Thr	Leu	Pro	Ser
			100					105					110		
Arg	Trp	Pro	Cys	Lys	Ala	Asp	Phe	Ala	Asp	Gly	Val	Gln	Ser	Leu	
		115					120					125			
Leu	Thr	Gln	Lys	Trp	Trp	Gly	Asp	Met	Ala	Ser	Thr	Thr	Pro	Ile	Trp
	130					135					140				
Ala	Leu	Val	Ile	Ala	Phe	Cys	Pro	Pro	Leu	Ile	Tyr	Thr	Arg	Leu	
145					150				155					160	
Ile	Thr	Phe	Arg	Lys	Ser	Glu	Glu	Glu	Pro	Thr	Arg	Glu	Glu	Leu	Glu
			165						170					175	
Phe	Asp	Met	Asp	Ser	Val	Ile	Asn	Gly	Glu	Gly	Pro	Val	Gly	Thr	Ala
		180						185					190		
Asp	Pro	Ala	Glu	Lys	Thr	Pro	Leu	Gly	Val	Pro	Arg	Gln	Ser	Gly	Arg
		195					200					205			
Pro	Gly	Cys	Cys	Gly	Gly	Arg	Cys	Gly	Gly	Arg	Arg	Cys	Leu	Arg	Arg
	210					215					220				
Trp	Phe	His	Phe	Trp	Gly	Ala	Pro	Val	Thr	Ile	Phe	Met	Gly	Asn	Val
225					230					235				240	
Val	Ser	Tyr	Leu	Leu	Phe	Leu	Leu	Leu	Phe	Ser	Arg	Val	Leu	Leu	Val
			245						250					255	
Asp	Phe	Gln	Pro	Ala	Pro	Pro	Gly	Ser	Leu	Glu	Leu	Leu	Leu	Tyr	Phe
		260					265						270		
Trp	Ala	Phe	Thr	Leu	Leu	Cys	Glu	Met	Arg	Gln	Gly	Leu	Ser	Gly	Gly
		275					280					285			
Gly	Gly	Ser	Leu	Ala	Ser	Gly	Gly	Pro	Gly	Pro	Gly	His	Ala	Ser	Leu
	290					295					300				
Ser	Gln	Arg	Leu	Arg	Leu	Tyr	Leu	Ala	Asp	Ser	Trp	Asn	Gln	Cys	Asp
305					310					315				320	
Leu	Val	Ala	Leu	Thr	Cys	Phe	Leu	Leu	Gly	Val	Gly	Cys	Arg	Leu	Thr
			325						330					335	
Pro	Gly	Leu	Tyr	His	Leu	Gly	Arg	Thr	Val	Leu	Cys	Ile	Asp	Phe	Met
		340						345					350		
Val	Phe	Thr	Val	Arg	Leu	Leu	His	Ile	Phe	Thr	Val	Asn	Lys	Gln	Leu
		355					360					365			
Gly	Pro	Lys	Ile	Val	Ile	Val	Ser	Lys	Met	Met	Lys	Asp	Val	Phe	Phe
	370					375					380				
Phe	Leu	Phe	Phe	Leu	Gly	Val	Trp	Leu	Val	Ala	Tyr	Gly	Val	Ala	Thr
385					390					395				400	
Glu	Gly	Leu	Leu	Arg	Pro	Arg	Asp	Ser	Asp	Phe	Pro	Ser	Ile	Leu	Arg
			405						410					415	
Arg	Val	Phe	Tyr	Arg	Pro	Tyr	Leu	Gln	Ile	Phe	Gly	Gln	Ile	Pro	Gln
			420					425					430		



Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser Glu  
435 440 445  
Pro Gly Phe Trp Ala His Pro Gly Ala Gln Ala Gly Thr Cys Val  
450 455 460  
Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Leu Val Ile Phe Leu  
465 470 475 480  
Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe Ser  
485 490 495  
Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys Ala  
500 505 510  
Gln Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu Ala Pro  
515 520 525  
Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Leu Arg Gln Leu Cys  
530 535 540  
Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu His Phe  
545 550 555 560  
Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr Trp Glu  
565 570 575  
Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp Lys Arg  
580 585 590  
Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val Asp Leu  
595 600 605  
Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg Leu Lys  
610 615 620  
Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly Trp Val  
625 630 635 640  
Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly Pro Pro  
645 650 655  
Pro Pro Asp Leu Pro Gly Ser Lys Asp  
660 665

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu Arg Arg Val Phe Tyr  
1 5 10 15  
Arg Cys

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ser Asn Cys Ser Ser Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys Ala Cys  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Thr Leu Gly Pro Arg Trp Pro Arg Pro Leu Ser Ser Ser Pro Thr Cys  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Cys Ala Gly Asp Pro Gly Ala Pro Ser Arg Pro Pro Arg Pro Ser Ser  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Ser Ile Ser Gly Phe Thr Phe Leu Arg Lys Pro Ser Gly Ser Cys  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Cys Ser Ser Ser Ser Ser Cys Ser Trp Pro Thr Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ala Lys Tyr Arg Ala Thr Ala Ile Ser Thr Gly Arg Arg Arg Leu Pro  
1 5 10 15  
Pro His Pro Cys  
20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Asp Tyr Lys Asp Asp Asp Asp Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Met His Thr Glu His  
1 5 10 15  
His His His His His  
20